



Does Not Comply
Corrected Diskette Needed

OICE

RAW SEQUENCE LISTING

DATE: 10/22/2002

PATENT APPLICATION: US/09/966,264C

TIME: 09:29:03

Input Set : N:\Crf4\10082002\I966264A.raw

Output Set: N:\CRF4\10222002\I966264C.raw

1 <110> APPLICANT: Barber, Elizabeth K
2 <120> TITLE OF INVENTION: Gene Expression Control Element DNA
3 <130> FILE REFERENCE: 896034605001
C--> 4 <140> CURRENT APPLICATION NUMBER: US/09/966,264C
5 <141> CURRENT FILING DATE: 2001-09-28
6 <150> PRIOR APPLICATION NUMBER: US 60/237,079
7 <151> PRIOR FILING DATE: 2000-09-30
8 <160> NUMBER OF SEQ ID NOS: 61
9 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

566 <210> SEQ ID NO: 51
567 <211> LENGTH: 1236
568 <212> TYPE: DNA
569 <213> ORGANISM: human
570 <400> SEQUENCE: 51

E--> 571	tag ttt cct att caa tgt ata gtg cac caa agg tca att caa gag	-192
572	Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu	
573	-75 -70 -65	
E--> 574	ttt att att att att ttc aac cca agt aaa agc aga gag aaa ata gcc	-144
575	Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala	
576	-60 -55 -50	
E--> 577	acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg	-96
578	Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu	
579	-45 -40 -35	
E--> 580	aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc	-48
581	Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr	
582	-30 -25 -20	
E--> 583	tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg gat ggt	0
584	Trp Val Leu Val Met Val Val Val Val Lys Val Val Met Asp Gly	
585	-15 -10 -5	
E--> 586	gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag	48
587	Val Val Leu Ile Val Lys Lys Met Phe Val Asn Thr Ser Arg Glu	
588	1 5 10 15	
E--> 589	taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc	96
590	Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro	
591	20 25 30	
E--> 592	atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga	144
593	Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly	
594	35 40 45	
E--> 595	att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat	192

cannot use negative
numbers or
See § 1.822(c)(6)
of the new Rules
37 CFR Part 1

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```

596   Ile Leu Leu Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Val Ala   His
597           50           55           60
E--> 598   ttt tcc atg taa aca cca gta gcc tga tcc aac att aag ctg ata cta 240
599   Phe Ser Met      Thr Pro Val Ala      Ser Asn Ile Lys Leu Ile Leu
600           65           70           75
E--> 601   aca aac aac gtg taa tgg ctt cat taa taa ggc ttt gct tct tcc tgg 288
602   Thr Asn Asn Val      Trp Leu His      Gly Phe Ala Ser Ser Trp
603           80           85
E--> 604   aaa ctg gtg aaa aat caa acc ttg ttg tgt aca ccc tcg atg cag ctt 336
605   Lys Leu Val Lys Asn Gln Thr Leu Leu Cys Thr Pro Ser Met Gln Leu
606           90           95           100
E--> 607   ctg tgt tgt ctt cac cca gaa atg ggg aat gat ttc cca aat ggc aaa 384
608   Leu Cys Cys Leu His Pro Glu Met Gly Asn Asp Phe Pro Asn Gly Lys
609   105           110           115           120
E--> 610   gaa aca gag tga tgc tat cta tct gca cct ttt gta aag tct gtc ttt 432
611   Glu Thr Glu      Cys Tyr Leu Ser Ala Pro Phe Val Lys Ser Val Phe
612           125           130           135
E--> 613   ctt tct ctt tgt ttt cca gga cac aat gta gga agt ctt ttc cac atg 480
614   Leu Ser Leu Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met
615           140           145           150
E--> 616   gca gat gat ttg ggc aga gcg atg gag tcc tta gta tca gtc atg aca 528
617   Ala Asp Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr
618           155           160           165
E--> 619   gat gaa gaa gga gca gaa taa atg ttt tac aac tcc tga ttc ccg cat 576
620   Asp Glu Glu Gly Ala Glu      Met Phe Tyr Asn Ser      Phe Pro His
621           170           175           180
E--> 622   ggt ttt tat aat att cat aca aca aag agg att aga cag taa gag ttt 624
623   Gly Phe Tyr Asn Ile His Thr Thr Lys Arg Ile Arg Gln      Glu Phe
624           185           190           195
E--> 625   aca aga aat aaa tct ata ttt ttg tga agg gta gtg gta tta tac tgt 672
626   Thr Arg Asn Lys Ser Ile Phe Leu      Arg Val Val Val Leu Tyr Cys
627           200           205           210
E--> 628   aga ttt cag tag ttt cta agt ctg tta ttg ttt tgt taa caa tgg cag 720
629   Arg Phe Gln      Phe Leu Ser Leu Leu Leu Phe Cys      Gln Trp Gln
630           215           220           225
E--> 631   gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca 768
632   Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr
633           230           235           240
E--> 634   tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg 816
635   Cys Lys Ile Leu Ile Ala Lys      Leu Ala Ile Ser Leu Tyr Gly Thr
636           245           250           255
E--> 637   cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat 864
638   His Phe Gly Leu Phe Lys Asn Leu      Gln Leu      Arg Lys Asn Tyr
639           260           265           270
E--> 640   aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act 912
641   Lys Gly Lys Arg Lys      Arg Asn Gly Gln Val Val Lys Leu      Thr
642           275           280
E--> 643   cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
644   Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys      Gly Arg

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```

645      285      290      295
E--> 646      aat agc atg aga agc cgt gtt tga tgt taa tta att      996
647      Asn Ser Met Arg Ser Arg Val      Cys      Leu Ile
E--> 648      300      305
701 <210> SEQ ID NO: 55
702 <211> LENGTH: 1236
703 <212> TYPE: DNA
704 <213> ORGANISM: human
705 <400> SEQUENCE: 55
706      ctagtttcct attcaatgta tagtgcacca aaggtcaatt caagagttta      50
707      ttattattat ttccaaccca agtaaaagca gagagaaaat agccacctcc      100
708      accatagcct cagaagcaag ccaacagcct gaaacagctt tgaaatgaaa      150
709      agttggtgtg gcggtgatgg tggcagtgat aatggtgacc gatggttggg      200
E--> 710      tgctggtgat ggtagtggtg gttgtgagag gtggtgatgg tggtttgatt      250
711      gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc      300
712      aatcactcat agccaagggtg gaaaagatgt atcccatcat ggaatattcc      350
713      tgttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat      400
714      ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag      450
715      tagcctgata caacattaag ctgatactaa caaacaacgt gtaatggctt      500
716      cattaataag gctttgcttc ttcctggaaa ctggtgaaaa atcaaacctt      550
717      gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg      600
718      ggaatgattt cccaaatggc aaagaaacag agtgatgcta tctatctgca      650
719      ccttttgtaa agtctgtctt tctttctctt tgttttccag gacacaatgt      700
720      aggaagtctt ttccacatgg cagatgattt gggcagagcg atggagtcct      750
721      tagtatcagt catgacagat gaagaaggag cagaataaat gttttacaac      800
722      tcctgattcc cgcattggtt ttataatatt catacaacaa agaggattag      850
E--> 723      acagtaagag tttaacaagaa ataaatcta ttttttgtg aagggtagtg      900
724      gtattatact gtagatttca gtagtttcta agtctgttat tgttttgtaa      950
725      acaatggcag gttttacacg tctatgcaat tgtacaaaaa agttataaga      1000
726      aaactacatg taaaatcttg atagctaaat aacttgccat ttctttatat      1050
727      ggaacgcatt ttgggttggt taaaaattta taacagttaa aaagaaagaa      1100
728      ttataaagga aaaagaaaat aacgcaatgg acaagtgggt aagctgtgaa      1150
729      ctgaggtgtg cacaattatc aggaacaccc caaaaccaa gtgaggtaga      1200
730      aatagcatga gaagccgtgt ttgatgttaa ttaatt      1236

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— must be represented
by a nucleotide

VERIFICATION SUMMARY

DATE: 10/22/2002

PATENT APPLICATION: US/09/966,264C

TIME: 09:29:04

Input Set : N:\Crf4\10082002\I966264A.raw

Output Set: N:\CRF4\10222002\I966264C.raw

L:4 M:270 C: Current Application Number differs, Wrong Format
L:571 M:254 E: No. of Bases conflict, LENGTH:Input:-192 Counted:46 SEQ:51
M:254 Repeated in SeqNo=51
L:648 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1236 Found:1237 SEQ:51
L:710 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:723 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1